

FIG. 1A

a Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln

b GGI GTC CCI TTC ATA TAA GTA GGI GT  
T T G G G  
T

c GGA GTC CCATTC ATA TA  
C T C T G  
T G T

d TTC ATA TAA GTA GGA GT  
T G G G C  
T G T

FIG. 1B

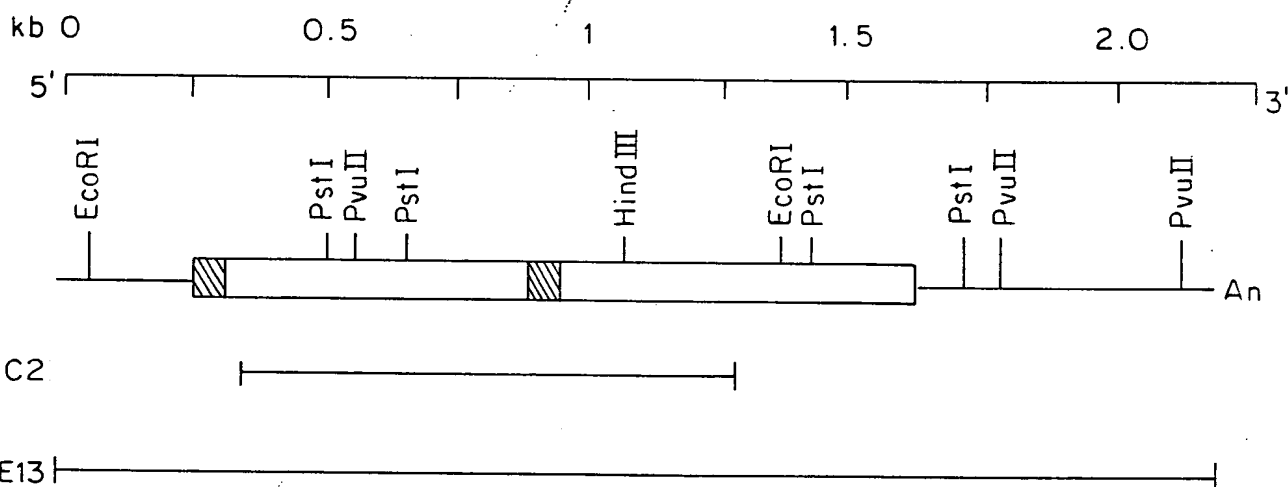
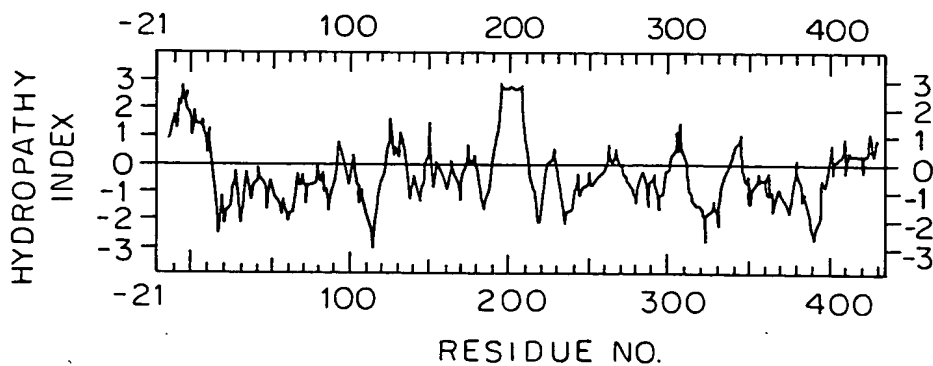


FIG. 1C



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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FIG. 1D(1)

18 ACCCAAAGGCCACAACCTGGAGCCTCAGTCCAGAGAATTCTGAGAAAATTAAAGCAGAGAGGGGAGAGATCACTGGGACCAGGCCGCGATCTCTATGCCCGAGTCTCAACCCCTCAA 136  
 137 CTGTCAACCCCAAGGCACCTTGGGACGTCTGGACAGACCGAGTCCCGGGAACCCCGAGTCCCGCTCCACACTGCCCTAGAGCCCAATGGGGGAGTGAGAGGCCATAGCTGTCTGGC 255

-21

-10

-1 +1

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Val Leu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu

256 ATG GGC CTC TCC ACC GTG CCT CAC CTG CTG CCG CTG GTG CTC CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG 345

\*

10

20

30

Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Ser Ile Cys Cys Thr

346 GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGG TGT ACC 435

40

50

60

Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr

436 AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC 525

70

80

90

Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp

526 GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TGC ACA GTG GAC 615

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FIG. 1D(2)

100 \_\_\_\_\_ 110 \_\_\_\_\_ 120 \_\_\_\_\_  
 Arg Asp Thr Val [CYS] Gly [CYS] Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln [CYS] Phe Asn [CYS] Ser Leu [CYS] Leu  
 616 CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC 705  
 130 \_\_\_\_\_ 140 \_\_\_\_\_ 150 \_\_\_\_\_  
 Asn Gly Thr Val His Leu Ser [CYS] Gln Glu Lys Gln Asn Thr Val [CYS] Thr [CYS] His Ala Gly Phe Phe Leu Arg Glu Asn Glu [CYS] Val  
 706 AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC 795  
 160 \_\_\_\_\_ 170 \_\_\_\_\_ 180 \_\_\_\_\_  
 Ser [CYS] Ser Asn [CYS] Lys Lys Ser Leu Glu [CYS] Thr Lys Leu [CYS] Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr  
 796 TCC TGT AGT AAC TGT AAG AAA AGC CTG CAG TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC 885  
 190 \_\_\_\_\_ 200 \_\_\_\_\_ 210 \_\_\_\_\_  
 Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu [CYS] Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
 886 ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT GGT CTT TGC CTT TTA TCC CTC CTC TTT ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG 975  
 220 \_\_\_\_\_ 230 \_\_\_\_\_ 240 \_\_\_\_\_  
 Ser Lys Leu Tyr Ser Ile Val [CYS] Gly Lys Ser Thr Pro Glu Lys Glu Gly Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn  
 976 TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA CAG GGG GAG CTT GAA GGA ACT ACT ACT AAG CCC CTG GCC CCA AAC 1065  
 250 \_\_\_\_\_ 260 \_\_\_\_\_ 270 \_\_\_\_\_  
 Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr  
 1066 CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTG GGC TTC AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC 1155

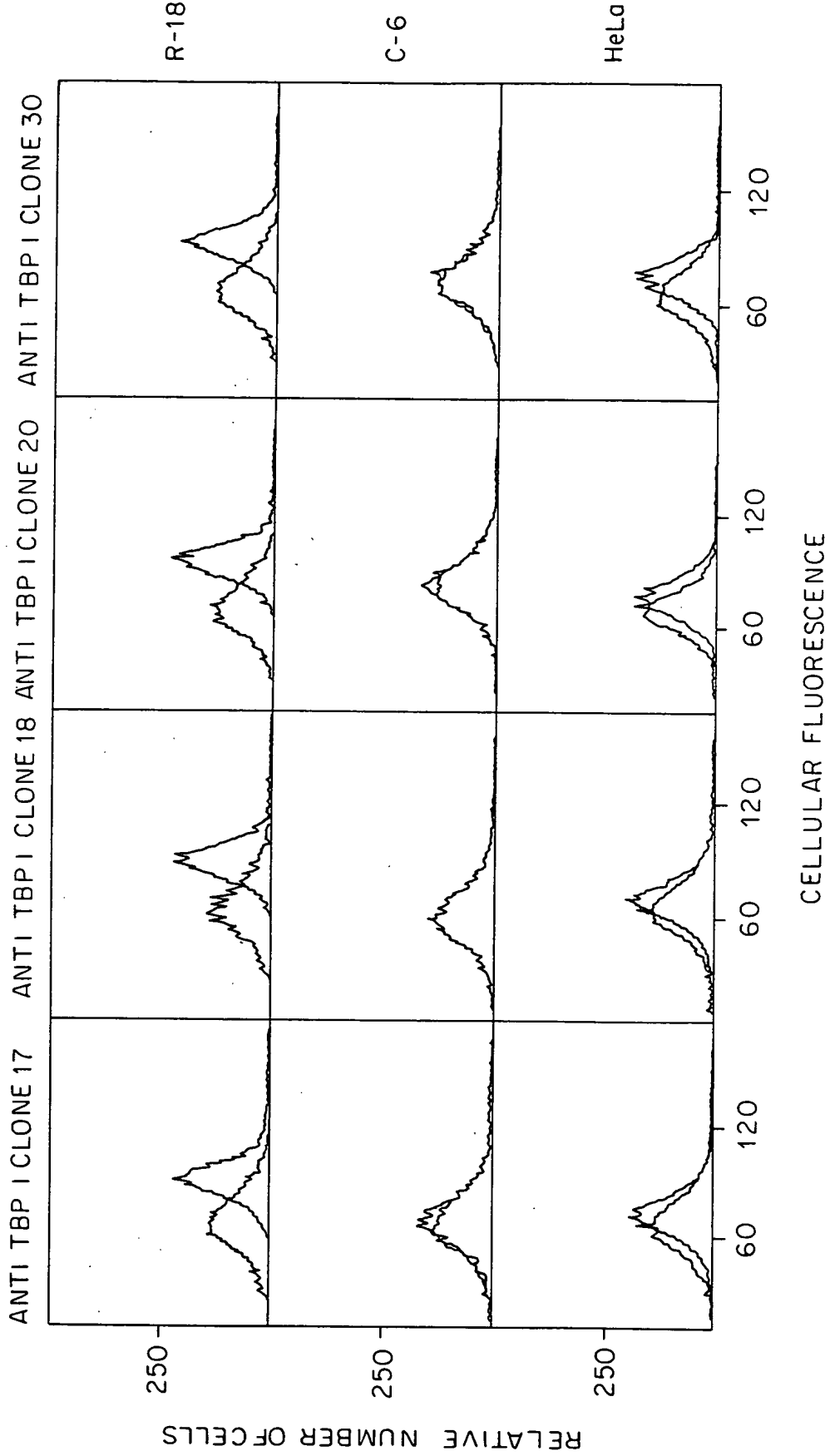
APPROVED	O.G. FIG.	
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# FIG. 1D(3)

280  
Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala  
1156 CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA CCA CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC 1245  
310  
Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Pro Ala Thr Leu Tyr  
1246 TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC 1335  
340  
Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu  
1336 GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CCC CTA GGG CTG AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG 1425  
370  
Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu  
1426 CAG AAC GGG CGC TGC CTG CGC GAG GCG CAA TAC AGC ATG CTG GCC ACC TGG AGG CGG CCC ACG CCG CGG GAG GCC ACG CTG GAG CTG 1515  
400  
Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala  
1516 CTG GGA CGC GTG CTC CGC GAC ATG GAC CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG CTT TGC GGC CCC GCC CTC CCG CCC GCG 1605  
430  
Pro Ser Leu Leu Arg End  
1606 CCC AGT CTT CTC AGA TGA GGCTGGCCCTCGGGCAGCTCTAAGGACCGTCCTGCGAGATCGCCTTCCAAACCCACCTTTTCTGGAAGAGGGTCTCTGCAGGGCAAGCA 1718  
1719 GGAGCTAGCAGCGCCCTACTTGGTGCTAAACCCCTCGATGTACATAGCTTTTCTCAGCTGCCTGCGCGCCGCCGACAGTACAGCGCTGTGCGCGCCGAGAGAGGTGCGCCGTGGCTCAAG 1837  
1838 AGCCTGAGTGGGTGGTTGCGAGGATGAGGACCGCTATGCCCTCATGCCCGTTTGGGTGTCTCACCAGCAAGGTGCTCGGGGGCCCCCTGGTTCTGCTCCCTGAGCCCTTTTTCACAGTGC 1956  
1957 ATAAGCAGTTTTTTTTTGTGTTTTTGTGTTTTTAAATCAATCATATGTTACACTATAGAAACCTTGGCACTCTCTGTCGCCCTCTGCTCGGACAGCATAGCAAGCTGAAC 2075  
2076 TGTCTAAGGCAGGGCGGACCACGGAACAATGGGGCCTTCAGCTGGAGCTGTGGACTTTTGTACATACACTAAATCTGAAAGTTAAAAAATAAAAAA 2175

APPROVED	O.G. FIG.	
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FIG. 2



APPROVED	O.G. FIG.	
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FIG. 3A

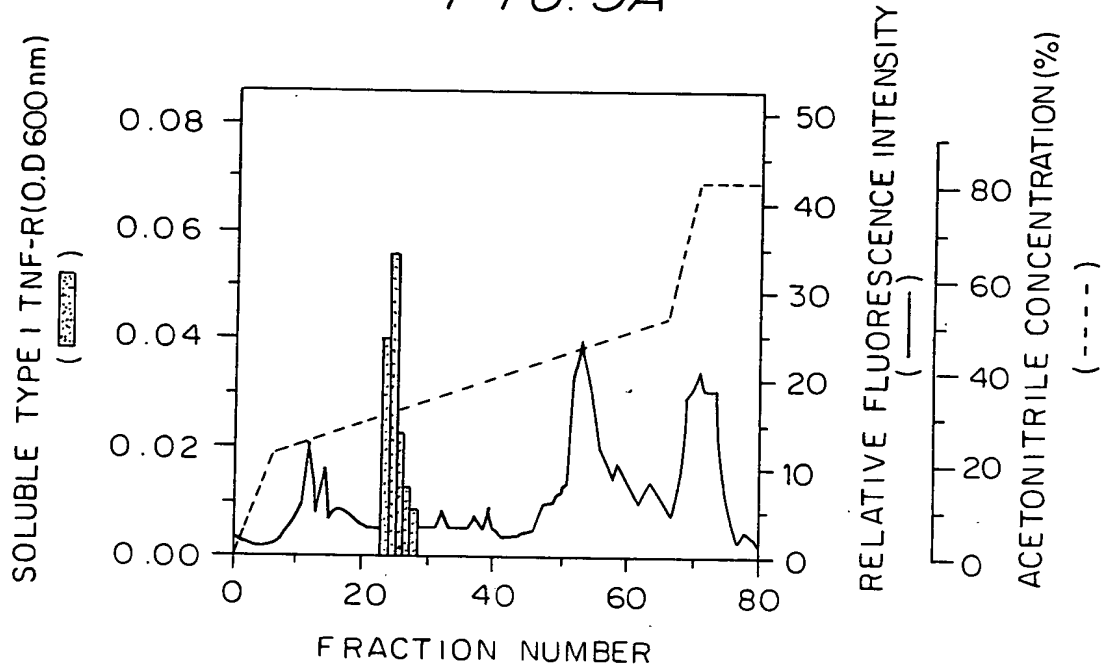
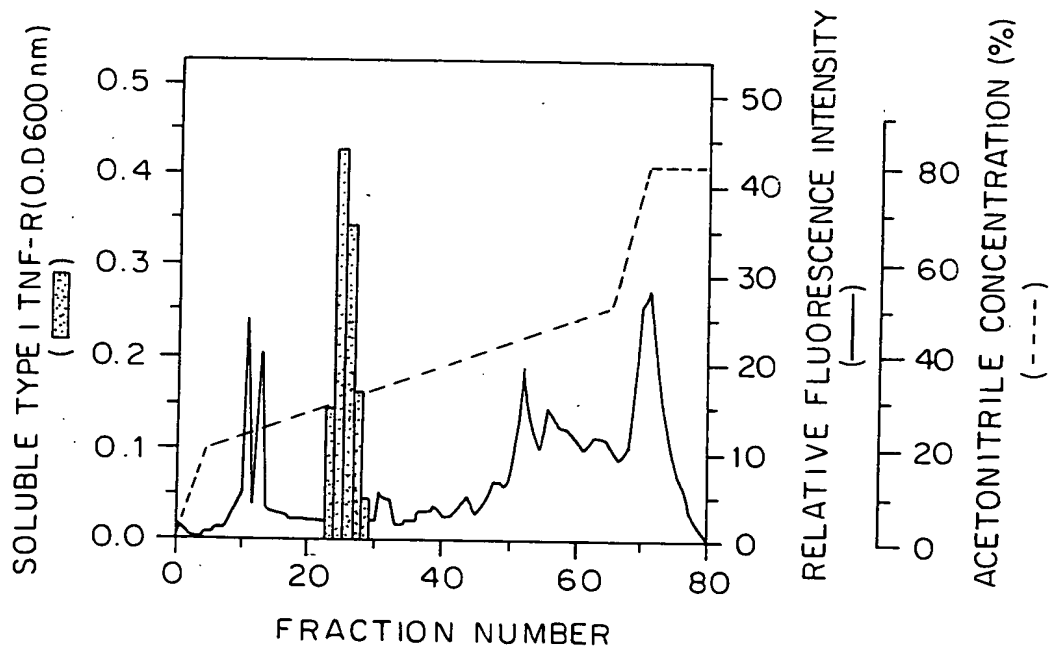
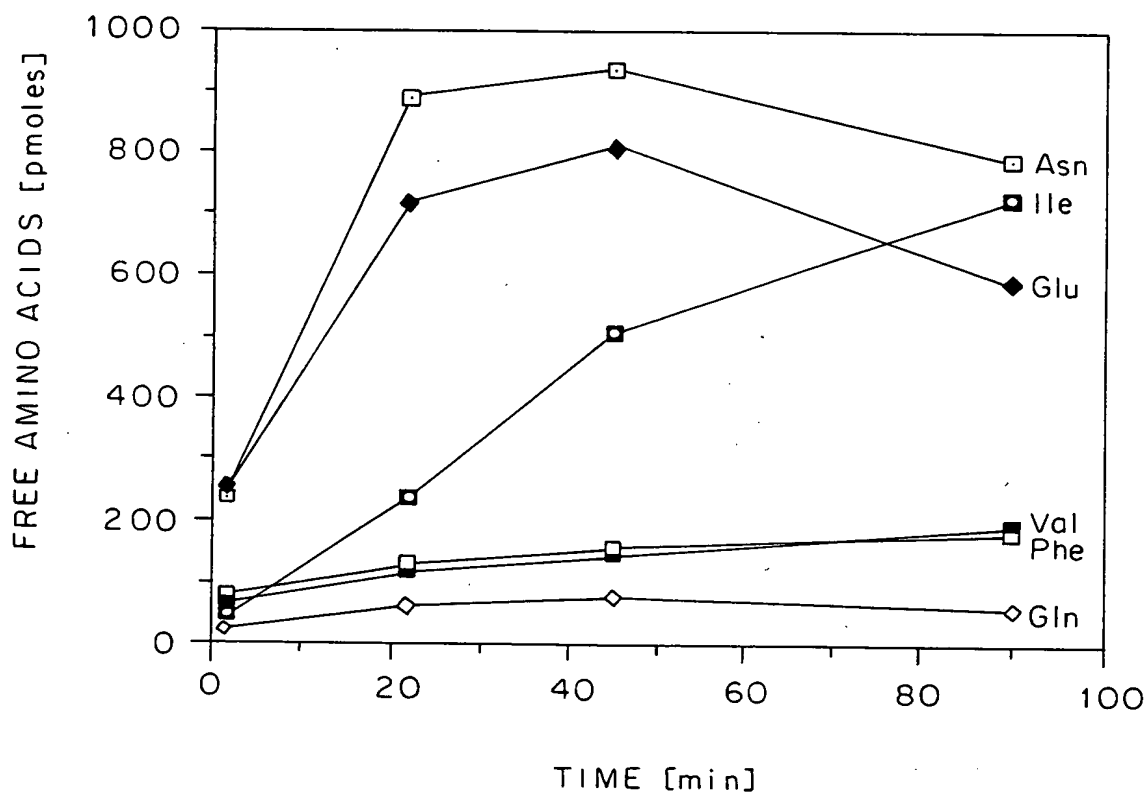


FIG. 3B



APPROVED	O.G. FIG.	
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FIG. 4



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 5A

CONSTRUCTION OF PLASMID pSV - TBP

-21  
 Met  
 ATG GGC CTC TCC ACC GTG CCT.....TGC CTA CCC CAG ATT GAG AAT  
 TAC CCG GAG AGG TGG CAC GGA.....ACG GAT GGG GTC TAA CTC TTA  
 5' 3'

180  
 Asu  
 TGC CTA CCC CAG ATT GAG AAT  
 TAA CTC TTA TGA TAA  
 3' 5'

PHOSPHORILATED 5' PRIMER  
 5' CCG CCG ATG GGC CTC TCC ACC GTG CCT .....  
 3' .....  
 PHOSPHORILATED 3' PRIMER  
 3' .....  
 5' CCG GAT GGG GTC TAA CTC TTA TGA TAA  
 3' .....

PCR AMPLIFICATION

615 bp FRAGMENT  
 ( CODING FOR TBP I INCLUDING  
 ITS SIGNAL PEPTIDE )

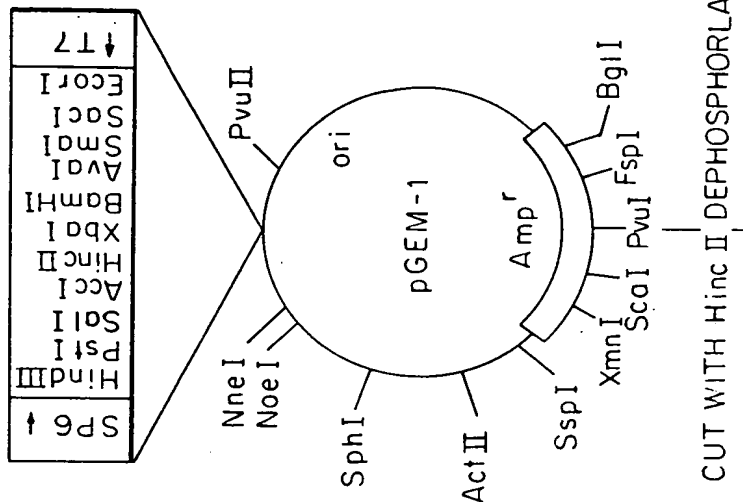
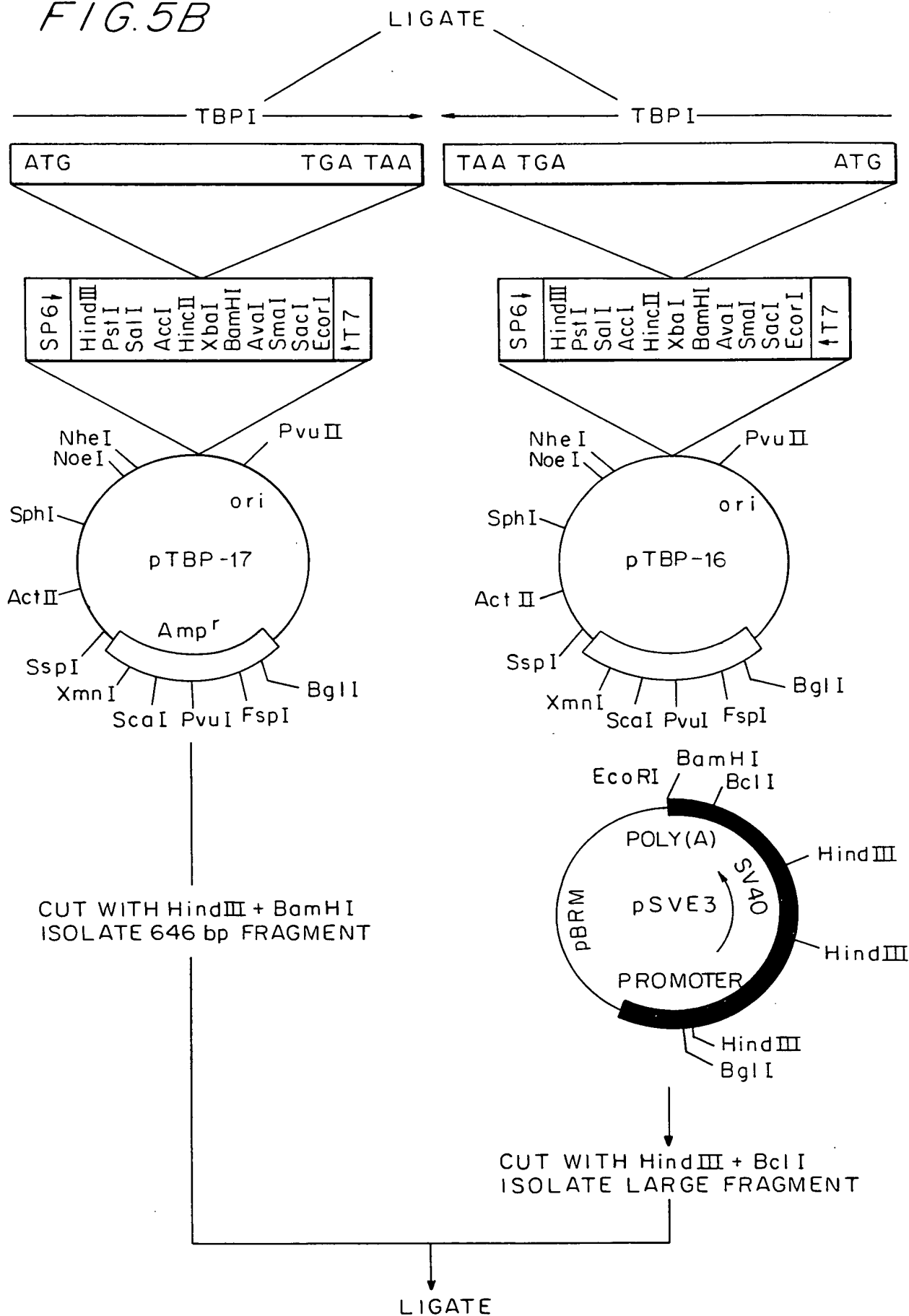


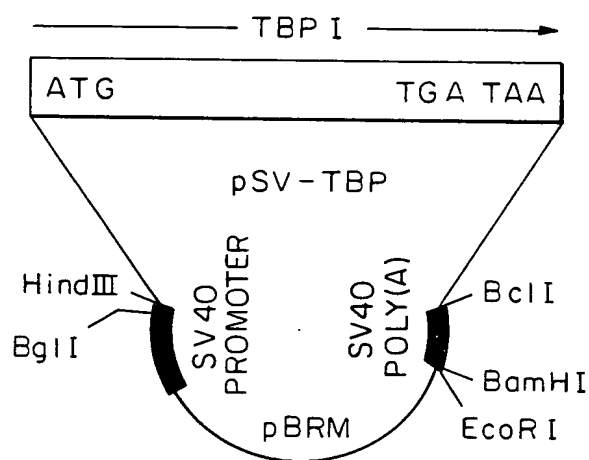


FIG. 5B



APPROVED	O.G. FIG.	
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FIG. 5C



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

# CONSTRUCTION OF PLASMID pCMV-TBP

FIG. 6A

## TNF RECEPTOR cDNA

-21  
Met

5'

3'

ATG GGC CTC TCC ACC GTG CCT.....TGC CTA CCC CAG ATT GAG AAT  
TAC CCG GAG AGG TGG CAC GGA.....ACG GAT GGG GTC TAA CTC TTA

180  
Asu

## PCR AMPLIFICATION

PHOSPHORILATED 5' PRIMER

5' CGG CCG ATG GGC CTC TCC ACC GTG CCT ..... ACG GAT GGG GTC TAA CTC TTA TGA TAA 5'  
3' .....  
PHOSPHORILATED 3' PRIMER

615 bp FRAGMENT

( CODING FOR TBP I INCLUDING  
ITS SIGNAL PEPTIDE )

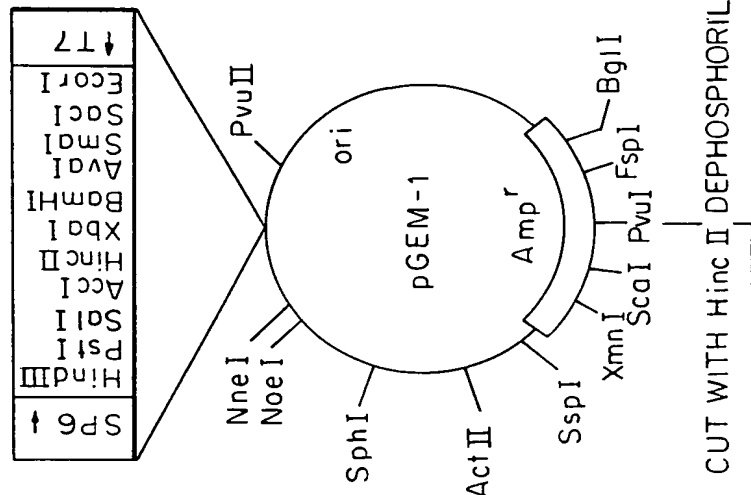
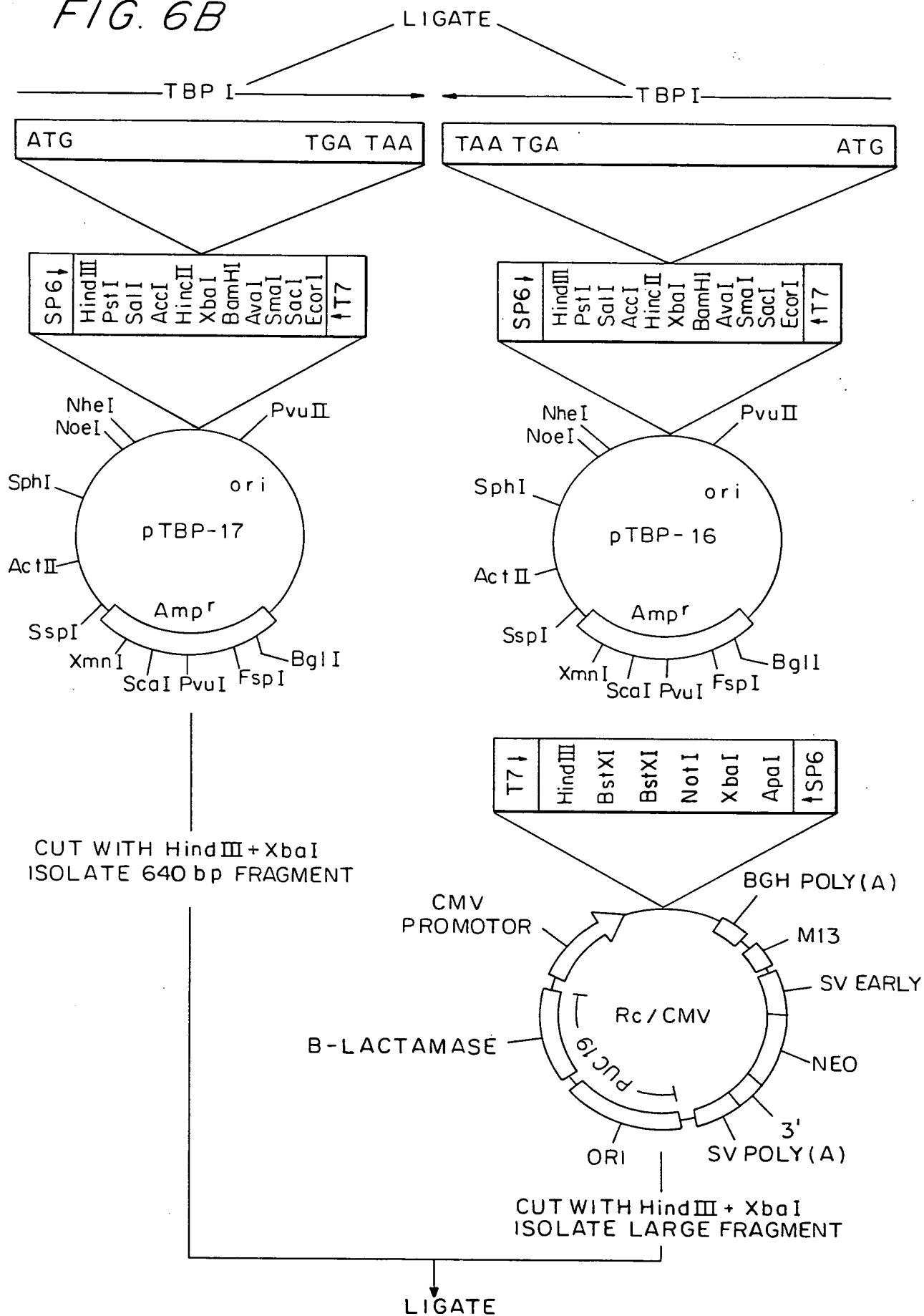


FIG. 6B



APPROVED	O.G. FIG.	
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FIG. 6C

